

09/646679

-1-

534 Rec'd PCT/PTG 20 SEP 2000  
SEQUENCE LISTING

<110> Wyatt, Paul  
Roberts, Jeremy A.  
Whitelaw, Catherine

<120> Signal Transduction Protein Involved in Plant Dehiscence

<130> 0623.0890000

<140> To Be Assigned

<141> Herewith

<150> GB9806113.8

<151> 1998-03-20

<160> 38

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: oligo dT primer 7

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14

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10

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PatentIn Ver. 2.0

19

18

26

29

23

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27

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<220>  
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<222> (20)..(427)

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1 5 10

ata aag aag aaa cta aac gtg ttg atc gtc gat gat gat cca cta aac 100  
Ile Lys Lys Lys Leu Asn Val Leu Ile Val Asp Asp Asp Pro Leu Asn  
15 20 25

ctt ata att cat gag aag atc atc aaa gcg att ggg ggt att tca cag 148  
Leu Ile Ile His Glu Lys Ile Ile Lys Ala Ile Gly Gly Ile Ser Gln  
30 35 40

aca gcg aat aac ggt gag gag gca gta atc atc cac cgt gac ggc ggc 196  
Thr Ala Asn Asn Gly Glu Glu Ala Val Ile Ile His Arg Asp Gly Gly  
45 50 55

tca tct ttt gac ctt atc cta atg gat aaa gaa atg ccc gag agg gat 244  
Ser Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp  
60 65 70 75

ggg gtt tcg aca act aag aag cta aga gaa atg gaa gtg aag tca atg 292  
Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Glu Val Lys Ser Met  
80 85 90

att gtt ggg gtg act tca ctg gct gac aat gaa gag gag cgc agg gct 340  
Ile Val Gly Val Thr Ser Leu Ala Asp Asn Glu Glu Glu Arg Arg Ala  
95 100 105

09645579 022004

ttc atg gaa gct gga ctt aac cat tgc ttg gca aaa ccg tta acc aag 388  
Phe Met Glu Ala Gly Leu Asn His Cys Leu Ala Lys Pro Leu Thr Lys  
110 115 120

gac aag atc atc cct ctc att aac caa ctc atg gat gct tgatggatat 437  
Asp Lys Ile Ile Pro Leu Ile Asn Gln Leu Met Asp Ala  
125 130 135

atattttata ttatggaaac acacataata acgtctaagt gtgtatgtat gcatagatac 497

ttgcatgtgt gtgttttaga atttaggggtt ctttatcgtc cgtgatatat aatcatgtaa 557

gttggttgctt taagcttata aaatatttaa ataagggttt cctctacc 605

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<212> PRT  
<213> Brassica napus

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Lys Ile Ile Lys Ala Ile Gly Gly Ile Ser Gln Thr Ala Asn Asn Gly  
35 40 45  
Glu Glu Ala Val Ile Ile His Arg Asp Gly Gly Ser Ser Phe Asp Leu  
50 55 60  
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr  
65 70 75 80  
Lys Lys Leu Arg Glu Met Glu Val Lys Ser Met Ile Val Gly Val Thr  
85 90 95  
Ser Leu Ala Asp Asn Glu Glu Glu Arg Arg Ala Phe Met Glu Ala Gly  
100 105 110  
Leu Asn His Cys Leu Ala Lys Pro Leu Thr Lys Asp Lys Ile Ile Pro  
115 120 125  
Leu Ile Asn Gln Leu Met Asp Ala  
130 135

<210> 16  
<211> 136  
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192220"6294560

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<210> 22
<211> 111
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> Unsure
<222> 67
<223> Xaa= any amino acid
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			20					25					30			
Asn	Glu	Glu	Cys	Leu	Arg	Val	Val	Ser	His	Glu	His	Lys	Val	Val	Phe	
		35					40					45				
Met	Asp	Val	Cys	Met	Pro	Gly	Val	Glu	Asn	Tyr	Gln	Ile	Ala	Leu	Arg	
	50					55					60					
Ile	His	Xaa	Pro	Leu	Leu	Val	Ala	Leu	Ser	Gly	Asn	Thr	Asp	Lys	Ser	
65					70					75					80	
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caaaaaaaaa  aaaaacnttt  tataatntca  ctatgagcaa  ttattccttat  agtggttttct  180
ttttccagaa  atttgacgac  aacctaacta  aaacaattta  atttgacggt  agttaagtaa  240
tttatataga  tggataaatt  gagcaagcac  attacgaact  gcggatcaag  gagagtcaca  300
atttaattct  tacgttatac  acaaaattat  ctaaatacta  tatatatata  cagctgcatg  360
ctacgataat  gatcaaagt  ttatgtactt  ttcagcgaaa  attcttgtcg  ccatacatta  420
ctgtgttaat  gaatcattaa  atatgtgaag  gaggaaaaga  gtacaaaagg  agttttgttg  480
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aggcatttcg	cagacactga	aatgtgaata	ataataaagg	aattgccgaa	ttgatttcta		540
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tnatattatc	actntggaca	ttagtnngat	agaccctagc	taaaattttt	aaaaattata		660
cattcatttt	ctnaagtacc	aaacttaatt	atcacaatcg	gataaaattg	tttaagaaac		720
cattacaaac	tcagcttgtg	gactctgaga	gaaactaaga	gctagacata	cggttagtag		780
tgtagccgca	ttttttatgc	ttaatttgct	taagcatgac	ttctatgctc	cttgatgata		840
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accattagct	caacaaacaa	aatactgaaa	gtatataatc	ttggttacag	aattcttatg		960
cAAAAAAtAT	cataatatat	atagaattcg	gttatgatta	agatgaatta	tttaattaat		1020
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ggtgtcatat	tagtttgGTA	agacaactca	gttgcaacga	tgcagattac	atttcaggaa		1140
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tcaactataa	atttcgatcg	atgtatctac	gttctttaaca	caattcacaa	tcttcttttag		1260
aatccAAAAT	tgtaagccgc	tttctaattct	ctttctcagt	atacatatgt	aatatgtatg		1320
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tcataacaaa	cacaaaaaaaa	catacgcacg	cattagaaca	cttgatgttt	aatttccata		1440
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aaa acc aag tca gta gaa gtg aag aag aaa ctt aac gtg ttg atc gtt							1599
Lys Thr Lys Ser Val Glu Val Lys Lys Lys Leu Asn Val Leu Ile Val							
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gat gat gat aca gta att cgt aaa ctt cac gag aat atc atc aaa tcg							1647
Asp Asp Asp Thr Val Ile Arg Lys Leu His Glu Asn Ile Ile Lys Ser							
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atc ggt gga att tca cag acg gct aag aac ggt gag gag gca gtg aac							1695
Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Asn							
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Ile His Arg Asp Gly Asn Ala							
	65						

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Val Ile Arg Lys Leu His Glu Asn Ile Ile Lys Ser Ile Gly Gly Ile
      35                          40                        45
Ser Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Asn Ile His Arg Asp
    50                          55                        60
Gly Asn Ala
    65
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catctttcga ccttatccta atggataaag aaatgcccg gagggatgga ctttcggcaa 180
ctaagaagct aagagaaatg aaagtgacgt ctatgattat tggggtgacg aactgggctg 240
acaatgaaga ggaacgtaag gctttcatgg aagctggact taaccattgc ttggcaaaac 300
ccttaagcaa agccaagatc ctccctctca tcaacaatct catggatgct tgatggatgg 360
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catacacctg tgtgtgtatg catagatatc tatccgcatg tgtgttttta gggttgttat 480
gtttgatttt tattgtgcgt ggcgtgatat acaatcangt nagtcgttac ttttggctta 540
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576

<210> 26  
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<212> PRT  
<213> Brassica napus

<220>  
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Asn Ile His Arg Asp Gly Asn Ala Ser Phe Asp Leu Ile Leu Met Asp  
35 40 45  
Lys Glu Met Pro Glu Arg Asp Gly Leu Ser Ala Thr Lys Lys Leu Arg  
50 55 60  
Glu Met Lys Val Thr Ser Met Ile Ile Gly Val Thr Thr Leu Ala Asp  
65 70 75 80  
Asn Glu Glu Glu Arg Lys Ala Phe Met Glu Ala Gly Leu Asn His Cys  
85 90 95  
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100 105 110  
Leu Met Asp Ala  
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<210> 27  
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<222> (180)..(605)

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tcattttttaa cttacttctt tttttttggt gaagattctt gagagaaaag aaatcgaag 179

atg gca aca aaa tcc acc gga ggt acc gag aaa acc aag tcg ata gaa 227
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
  1             5             10             15

gtg aag aag aaa cta atc aac gtg ttg atc gtc gat gat gat cca tta 275
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
          20             25             30

aac cgt aga ctc cac gag atg atc atc aaa acg atc gga gga att tct 323
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser
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cag act gca aag aat ggc gaa gag gcn gtg atc ctc cac cgt gac ggc 371
Gln Thr Ala Lys Asn Gly Glu Glu Xaa Val Ile Leu His Arg Asp Gly
          50             55             60

gaa gca tct ttc gac ctt att cta atg gat aag gaa atg cct gag agg 419
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg
          65             70             75             80

gat gga gtt tcg aca att aag ang cta aga gaa atg aaa ggg acg tca 467
Asp Gly Val Ser Thr Ile Lys Xaa Leu Arg Glu Met Lys Gly Thr Ser
          85             90             95

atg atc gtt ggg gta acg tca gta gct gac caa gaa gaa gag cgt aag 515
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Arg Lys
          100             105             110

gct ttt atg gaa gct ggg ctc aac cat tgc ttg gaa aaa ccc tta acc 563
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr
          115             120             125

aag gcc aag atc ttc ccg ctc att agc cac ctc ttc gat gct 605
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala
          130             135             140

tgatggatga aggctcatta atgtatctat attttcaatc atgaaatcac ctacacgtgt 665

atttgacaca aaaatctgca tttgttgtga tatagggttt ctcatatcta tgtttgattt 725

attttcttat cgtccgaggt aaaatcatgc aagtcatttc ttttggctaa taaaatatta 785

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<222> 1142

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ttaacatgta tgtgggatat ttggctataa attatgtaaa aaatttcacg atagattggt 180

gaatttttga atttcgagtt aaaatatctt caaattacct cacatttaca aaaaggtaga 240

actgttgaaa aactaatgct ctataaaaaca ctagacaata acaaaatacg taatgcgtaa 300

agaacctaaa ttatgatttt atttatcttt cttccttttt ccgtgagtat aagccatttt 360

tcatagtaaa gcattacgaa tacgacattg aacactactg acatataaag tagtagattt 420

tgatgggtta acttgatgac ttaatttgct taagcatgaa cttcaatgct tttataaaag 480

tacttcatga gaatattcct cgttctatac tagcagaagg gttcgatagt gattttacaa 540

ccgttcaaca aaacctttta acccaaaaaa ccaaagaatg aaagtatcta aacttgatta 600

tacatttctt gtctaaatta tcaaataaca tactctcttt tgtttactta taaacgatat 660

gaaagaaata aataaaaaga acatagaatc ttattatgat ctagaagaat taattaaaga 720

aatatatata tatttttttt catttctact catgtttctt atacattctt taaatttggt 780

caccattttg atttacttgt tctcatatta gtttggtata caactcactt agaataatgt 840

agattacatt tcagccaaat tcatgtaaaa gatgcttttc tttgtgatgt ttttaaaatg 900

ctttcttttc actttttttc tttcttaact ataaatcttg atcgaatgcc taccttctta 960

gaacataaga tcttctttta aatccaaaat cgtaggccac tatttcatta tacttatgta 1020

atatatgtga tacagataca tntatatata aattaaacac gaaaccatac atgcacggtg 1080

tgatcacaca cgcacacaca tagaaacata aacacgcaat aatttctata cagtttaatt 1140

tcatttttaa cttacttctt tttttttggt gaagattctt gagagaaaag aaatcgaag 1199

atg gca aca aaa tcc acc gga ggt acc gag aaa acc aag tcg ata gaa 1247
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
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gtg aag aag aaa cta atc aac gtg ttg atc gtc gat gat gat cca tta 1295
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
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Asn Arg Arg Leu His Glu Cys His Gln
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aagattagcg tttcaaaccc cgaa atg gcc cgt tgt cat gga agt ctt gct      171
                Met Ala Arg Cys His Gly Ser Leu Ala
                        1                      5

att ttc tta tgc gtt ctt ttg atg ctc gct tgc tgc caa gct ttg agt      219
Ile Phe Leu Cys Val Leu Leu Met Leu Ala Cys Cys Gln Ala Leu Ser
  10                      15                      20                      25

agc aac gta gat gat gga tat ggt cat gaa gat gga agc ttc gaa acc      267
Ser Asn Val Asp Asp Gly Tyr Gly His Glu Asp Gly Ser Phe Glu Thr
                30                      35                      40

gat agt tta atc aag ctc aac aac gac gac gac gtt ctt acc ttg aaa      315
Asp Ser Leu Ile Lys Leu Asn Asn Asp Asp Asp Val Leu Thr Leu Lys
                45                      50                      55

agc tcc gat aga ccc act acc gaa tca tca act gtt agt gtt tcg aac      363
Ser Ser Asp Arg Pro Thr Thr Glu Ser Ser Thr Val Ser Val Ser Asn
                60                      65                      70

ttc gga gca aaa ggt gat gga aaa acc gat gat act cag gct ttc aag      411
Phe Gly Ala Lys Gly Asp Gly Lys Thr Asp Asp Thr Gln Ala Phe Lys
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aaa gca tgg aag aag gca tgt tca aca aat gga gtg act act ttc ttg      459

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Lys 90	Ala	Trp	Lys	Lys	Ala 95	Cys	Ser	Thr	Asn	Gly 100	Val	Thr	Thr	Phe	Leu 105	
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cca Pro	tgc Cys	aaa Lys	tca Ser	tta Leu	cgt Arg	agc Ser	ttc Phe	cag Gln	atc Ile	cta Leu	ggc Gly	act Thr	tta Leu	tca Ser	gct Ala	555
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	155					160					165					
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aaa Lys	tct Ser	aag Lys	cca Pro	tgc Cys	aca Thr	aaa Lys	gcg Ala	cca Pro	acg Thr	gct Ala	ctt Leu	act Thr	ctc Leu	tac Tyr	aac Asn	747
				190					195					200		
cta Leu	aac Asn	aat Asn	ttg Leu	aat Asn	gtg Val	aag Lys	aat Asn	ctg Leu	aga Arg	gtg Val	aga Arg	aat Asn	gca Ala	cag Gln	cag Gln	795
			205					210					215			
att Ile	cag Gln	att Ile	tcg Ser	att Ile	gag Glu	aaa Lys	tgc Cys	aac Asn	agt Ser	gtt Val	gat Asp	gtt Val	aag Lys	aat Asn	gtt Val	843
		220					225					230				
aag Lys	atc Ile	act Thr	gct Ala	cct Pro	ggc Gly	gat Asp	agt Ser	ccc Pro	aac Asn	acg Thr	gat Asp	ggt Gly	att Ile	cat His	atc Ile	891
	235					240					245					
gtt Val 250	gct Ala	act Thr	aaa Lys	aac Asn	att Ile	cga Arg	atc Ile	tcc Ser	aat Asn	tca Ser	gac Asp	att Ile	ggg Gly	aca Thr	ggt Gly	939
					255					260					265	
gat Asp	gat Asp	tgc Cys	ata Ile	tcc Ser	att Ile	gag Glu	gat Asp	gga Gly	tcg Ser	caa Gln	aat Asn	gtt Val	caa Gln	atc Ile	aat Asn	987
				270					275					280		
gat Asp	tta Leu	act Thr	tgc Cys	ggc Gly	ccc Pro	ggt Gly	cat His	ggc Gly	atc Ile	agc Ser	att Ile	gga Gly	agc Ser	ttg Leu	ggg Gly	1035
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gat Asp	gac Asp	aat Asn	tcc Ser	aaa Lys	gct Ala	tat Tyr	gta Val	tcg Ser	gga Gly	att Ile	aat Asn	gtg Val	gat Asp	ggt Gly	gct Ala	1083
		300					305					310				
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Thr	Leu	Ser	Glu	Thr	Asp	Asn	Gly	Val	Arg	Ile	Lys	Thr	Tyr	Gln	Gly	
315						320					325					
ggg	tca	gga	act	gct	aag	aac	att	aaa	ttc	caa	aac	att	cgt	atg	gat	1179
Gly	Ser	Gly	Thr	Ala	Lys	Asn	Ile	Lys	Phe	Gln	Asn	Ile	Arg	Met	Asp	
330					335				340						345	
aat	gtc	aag	aat	ccg	atc	ata	atc	gac	cag	aac	tac	tgc	gac	aag	gac	1227
Asn	Val	Lys	Asn	Pro	Ile	Ile	Ile	Asp	Gln	Asn	Tyr	Cys	Asp	Lys	Asp	
				350				355						360		
aaa	tgc	gaa	caa	caa	gaa	tct	gcg	gtt	caa	gtg	aac	aat	gtc	gtg	tat	1275
Lys	Cys	Glu	Gln	Gln	Glu	Ser	Ala	Val	Gln	Val	Asn	Asn	Val	Val	Tyr	
			365					370						375		
cgg	aac	ata	caa	ggt	acg	agc	gca	acg	gat	gtg	gcg	ata	atg	ttt	aat	1323
Arg	Asn	Ile	Gln	Gly	Thr	Ser	Ala	Thr	Asp	Val	Ala	Ile	Met	Phe	Asn	
		380					385					390				
tgc	agt	gtg	aaa	tat	cca	tgc	caa	ggt	att	gtg	ctt	gag	aat	gtg	aac	1371
Cys	Ser	Val	Lys	Tyr	Pro	Cys	Gln	Gly	Ile	Val	Leu	Glu	Asn	Val	Asn	
		395				400					405					
atc	aaa	gga	gga	aaa	gct	tct	tgc	aaa	aat	gtc	aat	gtt	aag	gat	aaa	1419
Ile	Lys	Gly	Gly	Lys	Ala	Ser	Cys	Lys	Asn	Val	Asn	Val	Lys	Asp	Lys	
410					415				420					425		
ggc	acc	gtt	tct	cct	aaa	tgc	cct	taattactaa	gttgattatg	taatatacat						1473
Gly	Thr	Val	Ser	Pro	Lys	Cys	Pro									
				430												
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gatatatata	gaaaactaag	gatttatggg	aatatacata	caatagttga	gataattggt											1593
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 Gly His Glu Asp Gly Ser Phe Glu Thr Asp Ser Leu Ile Lys Leu Asn  
 35 40 45  
 Asn Asp Asp Asp Val Leu Thr Leu Lys Ser Ser Asp Arg Pro Thr Thr

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Lys	Thr	Asp	Asp	Thr 85	Gln	Ala	Phe	Lys	Lys	Ala	Trp	Lys	Lys	Ala	Cys 95
Ser	Thr	Asn	Gly 100	Val	Thr	Thr	Phe	Leu 105	Ile	Pro	Lys	Gly	Lys	Thr	Tyr
Leu	Leu	Lys 115	Ser	Ile	Arg	Phe	Arg 120	Gly	Pro	Cys	Lys	Ser 125	Leu	Arg	Ser
Phe 130	Gln	Ile	Leu	Gly	Thr	Leu 135	Ser	Ala	Ser	Thr	Lys 140	Arg	Ser	Asp	Tyr
Ser 145	Asn	Asp	Lys	Asn 150	His	Trp	Leu	Ile	Leu	Glu 155	Asp	Val	Asn	Asn	Leu 160
Ser	Ile	Asp	Gly	Gly 165	Ser	Ala	Gly	Ile	Val	Asp	Gly	Asn	Gly	Lys	Ile 175
Trp	Trp	Gln 180	Asn	Ser	Cys	Lys	Ile	Asp 185	Lys	Ser	Lys	Pro	Cys	Thr	Lys
Ala	Pro	Thr 195	Ala	Leu	Thr	Leu	Tyr 200	Asn	Leu	Asn	Asn	Leu 205	Asn	Val	Lys
Asn 210	Leu	Arg	Val	Arg	Asn	Ala 215	Gln	Gln	Ile	Gln	Ile	Ser 220	Ile	Glu	Lys
Cys 225	Asn	Ser	Val	Asp 230	Val	Lys	Asn	Val	Lys	Ile 235	Thr	Ala	Pro	Gly	Asp 240
Ser	Pro	Asn	Thr	Asp 245	Gly	Ile	His	Ile	Val 250	Ala	Thr	Lys	Asn	Ile	Arg 255
Ile	Ser	Asn 260	Ser	Asp	Ile	Gly	Thr	Gly 265	Asp	Asp	Cys	Ile	Ser 270	Ile	Glu
Asp	Gly	Ser 275	Gln	Asn	Val	Gln	Ile 280	Asn	Asp	Leu	Thr	Cys 285	Gly	Pro	Gly
His 290	Gly	Ile	Ser	Ile	Gly	Ser 295	Leu	Gly	Asp	Asp	Asn 300	Ser	Lys	Ala	Tyr
Val 305	Ser	Gly	Ile	Asn 310	Val	Asp	Gly	Ala	Thr	Leu 315	Ser	Glu	Thr	Asp	Asn 320
Gly	Val	Arg	Ile	Lys 325	Thr	Tyr	Gln	Gly	Gly 330	Ser	Gly	Thr	Ala	Lys	Asn 335
Ile	Lys	Phe 340	Gln	Asn	Ile	Arg	Met	Asp 345	Asn	Val	Lys	Asn 350	Pro	Ile	Ile

Ile Asp Gln Asn Tyr Cys Asp Lys Asp Lys Cys Glu Gln Gln Glu Ser  
 355 360 365  
 Ala Val Gln Val Asn Asn Val Val Tyr Arg Asn Ile Gln Gly Thr Ser  
 370 375 380  
 Ala Thr Asp Val Ala Ile Met Phe Asn Cys Ser Val Lys Tyr Pro Cys  
 385 390 395 400  
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 Cys Lys Asn Val Asn Val Lys Asp Lys Gly Thr Val Ser Pro Lys Cys  
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 ggt ggc ttg gag aca gtt aaa gtc aaa ttg cca gct gtc att agc gcc 95  
 Gly Gly Leu Glu Thr Val Lys Val Lys Leu Pro Ala Val Ile Ser Ala  
 20 25 30  
 gac ttg cgg ctc aat gag ccg cgg tac gct act ctg ccc aat atc atg 143  
 Asp Leu Arg Leu Asn Glu Pro Arg Tyr Ala Thr Leu Pro Asn Ile Met  
 35 40 45  
 aag gcc aag aag aag ccc atc aaa aag ctc aca gcc aca gat gtc ggt 191  
 Lys Ala Lys Lys Lys Pro Ile Lys Lys Leu Thr Ala Thr Asp Val Gly  
 50 55 60  
 gtg gac ttg gcg cca cgt caa caa gtg ttg agc gta gaa gac ccg ccc 239  
 Val Asp Leu Ala Pro Arg Gln Gln Val Leu Ser Val Glu Asp Pro Pro  
 65 70 75  
 acc aga cag gct ggt tcc att gtg cct gat gtc gac act ctc atc acc 287  
 Thr Arg Gln Ala Gly Ser Ile Val Pro Asp Val Asp Thr Leu Ile Thr  
 80 85 90 95  
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 Lys Leu Lys Glu Lys Gly His Leu  
 100

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aaa tcc tct ggt tcg ggt ttt cag tcc cat cag gag ttt ctc tat ggt      95
Lys Ser Ser Gly Ser Gly Phe Gln Ser His Gln Glu Phe Leu Tyr Gly
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